

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/598,274

DATE: 02/07/2001
TIME: 16:21:29

Input Set : A:\SeqList09598274.txt
Output Set: N:\CRF3\02072001\I598274.raw

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TECH CENTER 16002000

#16
BLL 1635
2-23-01

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4 <110> APPLICANT: Werther, George Arthur
5      Wraight, Christopher John
6      Edmondson, Stephanie Ruth
8 <120> TITLE OF INVENTION: METHOD FOR THE PROPHYLAXIS AND/OR
9      TREATMENT OF MEDICAL DISORDERS
12 <130> FILE REFERENCE: AP32556 071838.0125
14 <140> CURRENT APPLICATION NUMBER: 09/598,274
15 <141> CURRENT FILING DATE: 2000-06-21
17 <150> PRIOR APPLICATION NUMBER: 60/140,345
18 <151> PRIOR FILING DATE: 1999-06-21
20 <160> NUMBER OF SEQ ID NOS: 20
22 <170> SOFTWARE: FastSEQ for Windows Version 3.0
24 <210> SEQ ID NO: 1
25 <211> LENGTH: 1433
26 <212> TYPE: DNA
27 <213> ORGANISM: Human
29 <220> FEATURE:
30 <221> NAME/KEY: polyA_signal
31 <222> LOCATION: (1416)...(1420)
33 <221> NAME/KEY: polyA_site
34 <222> LOCATION: (1433)...(1433)
36 <221> NAME/KEY: CDS
37 <222> LOCATION: (118)...(1104)
38 <223> OTHER INFORMATION: Insulin-like growth factor binding protein
39      (IGFBP-2)
41 <221> NAME/KEY: sig_peptide
42 <222> LOCATION: (118)...(234)
44 <221> NAME/KEY: mat_peptide
45 <222> LOCATION: (235)...(1101)
46 <223> OTHER INFORMATION: mature IGFBP-2
48 <400> SEQUENCE: 1
49      attcggggcg agggaggagg aagaagcgga ggaggcggt cccgctcgca gggcgtgca      60
50      cctgcccgcc cgccgctcg ctcgctcgcc cgccgcgccg cgctgccgac cgccagc atg      120
51                                     Met
54      ctg ccg aga gtg ggc tgc ccc gcg ctg ccg ctg ccg ccg ccg ctg      168
55      Leu Pro Arg Val Gly Cys Pro Ala Leu Pro Leu Pro Pro Pro Leu
56      -35 -30 -25
58      ctg ccg ctg ctg ccg ctg ctg ctg ctg cta ctg ggc gcg agt ggc ggc      216
59      Leu Pro Leu Leu Pro Leu Leu Leu Leu Leu Gly Ala Ser Gly Gly
60      -20 -15 -10
62      ggc ggc ggg gcg cgc gcg gag gtg ctg ttc cgc tgc ccg ccc tgc aca      264
63      Gly Gly Gly Ala Arg Ala Glu Val Leu Phe Arg Cys Pro Pro Cys Thr
64      -5 1 5 10
66      ccc gag cgc ctg gcc gcc tgc ggg ccc ccg ccg gtt gcg ccg ccc gcc      312
67      Pro Glu Arg Leu Ala Ala Cys Gly Pro Pro Pro Val Ala Pro Pro Ala
68      15 20 25
70      gcg gtg gcc gca gtg gcc gga ggc gcc cgc atg cca tgc gcg gag ctc      360

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71 Ala Val Ala Ala Val Ala Gly Gly Ala Arg Met Pro Cys Ala Glu Leu
72          30          35          40
74 gtc cgg gag ccg ggc tgc ggc tgc tgc tgc gtg tgc gcc cgg ctg gag      408
75 Val Arg Glu Pro Gly Cys Gly Cys Cys Ser Val Cys Ala Arg Leu Glu
76          45          50          55
78 ggc gag gcg tgc ggc gtc tac acc ccg cgc tgc ggc cag ggg ctg cgc      456
79 Gly Glu Ala Cys Gly Val Tyr Thr Pro Arg Cys Gly Gln Gly Leu Arg
80          60          65          70
82 tgc tat ccc cac ccg ggc tcc gag ctg ccc ctg cag gcg ctg gtc atg      504
83 Cys Tyr Pro His Pro Gly Ser Glu Leu Pro Leu Gln Ala Leu Val Met
84          75          80          85          90
86 ggc gag ggc act tgt gag aag cgc cgg gac gcc gag tat ggc gcc agc      552
87 Gly Glu Gly Thr Cys Glu Lys Arg Arg Asp Ala Glu Tyr Gly Ala Ser
88          95          100          105
90 ccg gag cag gtt gca gac aat ggc gat gac cac tca gaa gga ggc ctg      600
91 Pro Glu Gln Val Ala Asp Asn Gly Asp Asp His Ser Glu Gly Gly Leu
92          110          115          120
94 gtg gag aac cac gtg gac agc acc atg aac atg ttg ggc ggg gga ggc      648
95 Val Glu Asn His Val Asp Ser Thr Met Asn Met Leu Gly Gly Gly Gly
96          125          130          135
98 agt gct ggc cgg aag ccc ctc aag tgc ggt atg aag gag ctg gcc gtg      696
99 Ser Ala Gly Arg Lys Pro Leu Lys Ser Gly Met Lys Glu Leu Ala Val
100          140          145          150
102 ttc cgg gag aag gtc act gag cag cac cgg cag atg ggc aag ggt ggc      744
103 Phe Arg Glu Lys Val Thr Glu Gln His Arg Gln Met Gly Lys Gly Gly
104          155          160          165          170
106 aag cat cac ctt ggc ctg gag gag ccc aag aag ctg cga cca ccc cct      792
107 Lys His His Leu Gly Leu Glu Glu Pro Lys Lys Leu Arg Pro Pro Pro
108          175          180          185
110 gcc agg act ccc tgc caa cag gaa ctg gac cag gtc ctg gag cgg atc      840
111 Ala Arg Thr Pro Cys Gln Gln Glu Leu Asp Gln Val Leu Glu Arg Ile
112          190          195          200
114 tcc acc atg cgc ctt ccg gat gag cgg ggc cct ctg gag cac ctc tac      888
115 Ser Thr Met Arg Leu Pro Asp Glu Arg Gly Pro Leu Glu His Leu Tyr
116          205          210          215
118 tcc ctg cac atc ccc aac tgt gac aag cat ggc ctg tac aac ctc aaa      936
119 Ser Leu His Ile Pro Asn Cys Asp Lys His Gly Leu Tyr Asn Leu Lys
120          220          225          230
122 cag tgc aag atg tct ctg aac ggg cag cgt ggg gag tgc tgg tgt gtg      984
123 Gln Cys Lys Met Ser Leu Asn Gly Gln Arg Gly Glu Cys Trp Cys Val
124          235          240          245          250
126 aac ccc aac acc ggg aag ctg atc cag gga gcc ccc acc atc cgg ggg      1032
127 Asn Pro Asn Thr Gly Lys Leu Ile Gln Gly Ala Pro Thr Ile Arg Gly
128          255          260          265
130 gac ccc gag tgt cat ctc ttc tac aat gag cag cag gag gct tgc ggg      1080
131 Asp Pro Glu Cys His Leu Phe Tyr Asn Glu Gln Gln Glu Ala Cys Gly
132          270          275          280
134 gtg cac acc cag cgg atg cag tag accgcagcca gccggtgcct ggcgcccctg      1134
135 Val His Thr Gln Arg Met Gln *
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136          285
138 cccccgcgcc ctctccaaac accggcgagaa aacggagagt gcttgggtgg tgggtgctgg 1194
139 aggattttcc agttctgaca cacgtattta tatttgaaa gagaccagca ccgagctcgg 1254
140 caccctcccg gcctctctct tcccagctgc agatgccaca cctgctcctt cttgctttcc 1314
141 ccgggggagg aaggggggtg tggtcgggga gctgggggtac aggtttgggg agggggaaga 1374
142 gaaattttta tttttgaacc cctgtgtccc ttttgcataa gattaaagga aggaaaagt 1433
144 <210> SEQ ID NO: 2
145 <211> LENGTH: 2474
146 <212> TYPE: DNA
147 <213> ORGANISM: Human
149 <220> FEATURE:
150 <221> NAME/KEY: CDS
151 <222> LOCATION: (110)...(985)
152 <223> OTHER INFORMATION: Insulin-like growth factor-binding protein
153 (IGFBP-3)
155 <400> SEQUENCE: 2
156 ctcagegcgcc agccgcttcc tgccctggatt ccacagcttc gcgcgctgta ctgtcgcccc 60
157 atccctgcgc gccagcctg ccaagcagcg tgccccggtt gcaggcgtc atg cag cgg 118
158 Met Gln Arg
159 1
161 gcg cga ccc acg ctc tgg gcc gct gcg ctg act ctg ctg gtg ctg ctc 166
162 Ala Arg Pro Thr Leu Trp Ala Ala Leu Thr Leu Leu Val Leu Leu
163 5 10 15
165 cgc ggg ccg ccg gtg gcg cgg gct ggc gcg agc tcg ggg ggc ttg ggt 214
166 Arg Gly Pro Pro Val Ala Arg Ala Gly Ala Ser Ser Gly Gly Leu Gly
167 20 25 30 35
169 ccc gtg gtg cgc tgc gag ccg tgc gac gcg cgt gca ctg gcc cag tgc 262
170 Pro Val Val Arg Cys Glu Pro Cys Asp Ala Arg Ala Leu Ala Gln Cys
171 40 45 50
173 gcg cct ccg ccc gcc gtg tgc gcg gag ctg gtg cgc gag ccg ggc tgc 310
174 Ala Pro Pro Pro Ala Val Cys Ala Glu Leu Val Arg Glu Pro Gly Cys
175 55 60 65
177 ggc tgc tgc ctg acg tgc gca ctg agc gag ggc cag ccg tgc ggc atc 358
178 Gly Cys Cys Leu Thr Cys Ala Leu Ser Glu Gly Gln Pro Cys Gly Ile
179 70 75 80
181 tac acc gag cgc tgt ggc tcc ggc ctt cgc tgc cag ccg tcg ccc gac 406
182 Tyr Thr Glu Arg Cys Gly Ser Gly Leu Arg Cys Gln Pro Ser Pro Asp
183 85 90 95
185 gag gcg cga ccg ctg cag gcg ctg ctg gac ggc cgc ggg ctc tgc gtc 454
186 Glu Ala Arg Pro Leu Gln Ala Leu Leu Asp Gly Arg Gly Leu Cys Val
187 100 105 110 115
189 aac gct agt gcc gtc agc cgc ctg cgc gcc tac ctg ctg cca gcg ccg 502
190 Asn Ala Ser Ala Val Ser Arg Leu Arg Ala Tyr Leu Leu Pro Ala Pro
191 120 125 130
193 cca gct cca gga aat gct agt gag tcg gag gaa gac cgc agc gcc ggc 550
194 Pro Ala Pro Gly Asn Ala Ser Glu Ser Glu Glu Asp Arg Ser Ala Gly
195 135 140 145
197 agt gtg gag agc ccg tcc gtc tcc agc acg cac cgg gtg tct gat ccc 598
198 Ser Val Glu Ser Pro Ser Val Ser Ser Thr His Arg Val Ser Asp Pro

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199	150	155	160	
201	aag ttc cac ccc ctc cat tca aag ata atc atc atc aag aaa ggg cat	646		
202	Lys Phe His Pro Leu His Ser Lys Ile Ile Ile Lys Lys Gly His			
203	165 170 175			
205	gct aaa gac agc cag cgc tac aaa gtt gac tac gag tct cag agc aca	694		
206	Ala Lys Asp Ser Gln Arg Tyr Lys Val Asp Tyr Glu Ser Gln Ser Thr			
207	180 185 190 195			
209	gat acc cag aac ttc tcc tcc gag tcc aag cgg gag aca gaa tat ggt	742		
210	Asp Thr Gln Asn Phe Ser Ser Glu Ser Lys Arg Glu Thr Glu Tyr Gly			
211	200 205 210			
213	ccc tgc cgt aga gaa atg gaa gac aca ctg aat cac ctg aag ttc ctc	790		
214	Pro Cys Arg Arg Glu Met Glu Asp Thr Leu Asn His Leu Lys Phe Leu			
215	215 220 225			
217	aat gtg ctg agt ccc agg ggt gta cac att ccc aac tgt gac aag aag	838		
218	Asn Val Leu Ser Pro Arg Gly Val His Ile Pro Asn Cys Asp Lys Lys			
219	230 235 240			
221	gga ttt tat aag aaa aag cag tgt cgc cct tcc aaa ggc agg aag cgg	886		
222	Gly Phe Tyr Lys Lys Lys Gln Cys Arg Pro Ser Lys Gly Arg Lys Arg			
223	245 250 255			
225	ggc ttc tgc tgg tgt gtg gat aag tat ggg cag cct ctc cca ggc tac	934		
226	Gly Phe Cys Trp Cys Val Asp Lys Tyr Gly Gln Pro Leu Pro Gly Tyr			
227	260 265 270 275			
229	acc acc aag ggg aag gag gac gtg cac tgc tac agc atg cag agc aag	982		
230	Thr Thr Lys Gly Lys Glu Asp Val His Cys Tyr Ser Met Gln Ser Lys			
231	280 285 290			
233	tag acgcctgccc caagttaatg tggagctcaa atatgcctta ttttgcacaa	1035		
234	*			
W--> 237	aagactgccca aggacatgac cagcagctgg ctacagcctc gatttatatt tctgtttgtg	1095		
238	gtgaactgat tttttttaa ccaaagttaa gaaagaggtt tttgaaatgc ctatggtttc	1155		
239	tttgaatggt aaacttgagc atcttttcac ttccagtag tcagcaaaga gcagtttgaa	1215		
240	ttttctgtgc gcttctatc aaaatattca gagactcgag cacagcacc agacttcacg	1275		
241	cgcccgtgga atgctcacca catgttggtc gaagcggccg accactgact ttgtgactta	1335		
242	ggcggctgtg ttgcctatgt agagaacacg cttcaccccc actcccgcga cagtgcgcac	1395		
243	aggctttatc gagaatagga aaacctttta accccggtea tccggacatc coaacgcatg	1455		
244	ctcctggagc tcacagcctt ctgtggtgtc atttctgaaa caagggcgtg gatccctcaa	1515		
245	ccaagaagaa tgtttatgtc ttcaagtgtc ctgtactgct tggggactat tggagaaaat	1575		
246	aaggtggagt cctacttggt taaaaaatat gtatctaaga atgttctagg gcactctggg	1635		
247	aacctataaa ggcaggtatt togggcccctc ctcttcagga atcttctga agacatggcc	1695		
248	cagtcgaagg ccaggatgg cttttgctgc ggcgccgtgg ggtaggagg acagagagac	1755		
249	gggagagtca gctccacat tcagaggcat cacaagtaat ggcacaatc ttcggatgac	1815		
250	tgcagaaaaat agtggtttgt agttcaacaa ctcaagacga agcttatttc tgaggataag	1875		
251	ctcttttaaag gcaaagcttt attttcatot ctcatotttt gtcttcctta gcacaatgta	1935		
252	aaaaagaata gtaatatcag aacaggaagg aggaatggct tgctggggag cccatccagg	1995		
253	acactgggag cacatagaga ttcacccatg tttgttgaac ttagagtcac tctcatgctt	2055		
254	ttctttataa ttcacacata tatgcagaga agatatgttc ttgttaacat tgtatacaac	2115		
255	atagcccaa atatatgaag atctatacta gataatccta gatgaaatgt tagagatgct	2175		
256	atatgataca actgtggcca tgactgagga aaggagctca cgcccagaga ctggygtgct	2235		
257	ctcccggagg ccaaacccaa gaaggtctgg caaagtcagg ctgagygaga ctctgcctg	2295		
258	ctgcagacct cggtgtggac acacgctgca tagagctctc ottgaaaaca gaggggtctc	2355		

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259 aagacattct gcctacctat tagcttttct ttattttttt aacttttttg ggaggaaaagt 2415
260 atttttgaga agtttgtctt gcaatgtatt tataaatagt aaataaagtt ttaccatt 2474
262 <210> SEQ ID NO: 3
263 <211> LENGTH: 4989
264 <212> TYPE: DNA
265 <213> ORGANISM: Human
267 <220> FEATURE:
268 <221> NAME/KEY: sig_peptide
269 <222> LOCATION: (32)...(121)
271 <221> NAME/KEY: mat_peptide
272 <222> LOCATION: (122)...(4132)
274 <221> NAME/KEY: misc_feature
275 <222> LOCATION: (122)...(2251)
276 <223> OTHER INFORMATION: Alpha subunit
278 <221> NAME/KEY: misc_feature
279 <222> LOCATION: (182)...(190)
280 <223> OTHER INFORMATION: Potential N-linked glycosylation site
282 <221> NAME/KEY: misc_feature
283 <222> LOCATION: (335)...(343)
284 <223> OTHER INFORMATION: Potential N-linked glycosylation site
286 <221> NAME/KEY: misc_feature
287 <222> LOCATION: (434)...(442)
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290 <221> NAME/KEY: misc_feature
291 <222> LOCATION: (761)...(769)
292 <223> OTHER INFORMATION: Potential N-linked glycosylation site
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296 <223> OTHER INFORMATION: Potential N-linked glycosylation site
298 <221> NAME/KEY: misc_feature
299 <222> LOCATION: (1280)...(1288)
300 <223> OTHER INFORMATION: Potential N-linked glycosylation site
302 <221> NAME/KEY: misc_feature
303 <222> LOCATION: (1343)...(1351)
304 <223> OTHER INFORMATION: Potential N-linked glycosylation site
306 <221> NAME/KEY: misc_feature
307 <222> LOCATION: (1631)...(1639)
308 <223> OTHER INFORMATION: Potential N-linked glycosylation site
310 <221> NAME/KEY: misc_feature
311 <222> LOCATION: (1850)...(1858)
312 <223> OTHER INFORMATION: Potential N-linked glycosylation site
314 <221> NAME/KEY: misc_feature
315 <222> LOCATION: (1895)...(1903)
316 <223> OTHER INFORMATION: Potential N-linked glycosylation site
318 <221> NAME/KEY: misc_feature
319 <222> LOCATION: (1949)...(1957)
320 <223> OTHER INFORMATION: Potential N-linked glycosylation site
322 <221> NAME/KEY: misc_feature
323 <222> LOCATION: (2240)...(2251)

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VERIFICATION SUMMARY DATE: 02/07/2001
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Input Set : A:\SeqList09598274.txt
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L:237 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:2
L:386 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:390 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3